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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=1; day=24; hr=14; min=38; sec=20; ms=812; ]

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Application No: 10522513 Version No: 1.0

Input Set:

Output Set:

Started: 2008-01-15 15:36:47.666  
Finished: 2008-01-15 15:36:50.863  
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 197 ms  
Total Warnings: 52  
Total Errors: 0  
No. of SeqIDs Defined: 52  
Actual SeqID Count: 52

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (3)
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**Input Set:**

**Output Set:**

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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
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# SEQUENCE LISTING

<110> Brownlie, John  
Chalker, Victoria J.  
Erles, Kerstin

<120> CANINE RESPIRATORY CORONAVIRUS (CRCV) SPIKE PROTEIN, POLYMERASE AND  
HEMAGGLUTININ/ESTERASE

<130> ERP02.003APC

<140> 10522513

<141> 2008-01-15

<150> PCT/GB03/02832

<151> 2003-07-01

<150> GB 0217434.0

<151> 2002-07-27

<160> 52

<170> PatentIn version 3.1

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<212> DNA

<213> canine respiratory coronavirus

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<212> PRT

<213> canine respiratory coronavirus

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Ile Gly Thr Thr Lys Phe Tyr Gly Gly Trp Asp Asp Met Leu Arg Arg  
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Asn	Gly	Tyr	Tyr	Pro	Thr	Ser	Gly	Ser	Thr	Tyr	Arg	Asn	Met	Ala	Leu	65	70	75
Lys	Gly	Thr	Leu	Leu	Leu	Ser	Thr	Leu	Trp	Phe	Lys	Pro	Pro	Phe	Leu	85	90	95
Ser	Asp	Phe	Ile	Asp	Gly	Val	Phe	Ala	Lys	Val	Lys	Asn	Thr	Lys	Val	100	105	110
Ile	Lys	Asp	Gly	Val	Val	Tyr	Ser	Glu	Phe	Pro	Ala	Ile	Thr	Ile	Gly	115	120	125
Ser	Thr	Phe	Val	Asn	Thr	Ser	Tyr	Ser	Val	Val	Val	Gln	Pro	His	Thr	130	135	140
Thr	Asn	Leu	Asp	Asn	Lys	Leu	Gln	Gly	Leu	Leu	Glu	Ile	Ser	Val	Cys	145	150	155
Gln	Tyr	Thr	Met	Cys	Asp	Tyr	Pro	His	Thr	Met	Cys	His	Pro	Asn	Leu	165	170	175
Gly	Asn	Lys	Arg	Ile	Glu	Leu	Trp	His	Trp	Asp	Thr	Gly	Val	Val	Pro	180	185	190
Cys	Leu	Tyr	Lys	Arg	Asn	Phe	Thr	Tyr	Asp	Val	Asn	Ala	Asp	Tyr	Leu	195	200	205
Tyr	Ser	His	Phe	Tyr	Gln	Glu	Gly	Gly	Thr	Phe	Tyr	Ala	Tyr	Phe	Thr	210	215	220
Asp	Thr	Gly	Val	Val	Thr	Lys	Phe	Leu	Phe	His	Val	Tyr	Leu	Gly	Thr	225	230	235
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260 265 270

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275 280 285

Asp Phe Met Ser Glu Ile Lys Cys Lys Thr Leu Ser Ile Ala Pro Ser  
290 295 300

Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Ile Ala Asp  
305 310 315 320

Val Tyr Arg Arg Ile Pro Asn Leu Pro Asp Cys Asn Ile Glu Ala Trp  
325 330 335

Leu Asn Asp Lys Ser Val Pro Ser Pro Leu Asn Trp Glu Arg Lys Thr  
340 345 350

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355 360 365

Ala Asp Ser Phe Thr Cys Asn Asn Ile Asp Ala Ala Lys Ile Tyr Gly  
370 375 380

Met Cys Phe Phe Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Gly  
385 390 395 400

Arg Lys Val Asp Leu Gln Met Gly Asn Leu Gly Tyr Leu Gln Ser Phe  
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Asn Tyr Arg Ile Asp Thr Thr Ala Thr Ser Cys Gln Leu Tyr Tyr Asn  
420 425 430

Leu Pro Ala Ser Asn Val Ser Ile Ser Arg Phe Asn Pro Ser Ile Trp  
435 440 445

Asn Arg Arg Phe Gly Phe Thr Glu Gln Ser Val Phe Lys Pro Gln Pro  
450 455 460

Val Gly Val Phe Thr Asp His Asp Val Val Tyr Ala Gln His Cys Phe

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725 730 735

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Gly Ser Gly Tyr Trp Gly Asp Tyr Ser Thr Gln Arg Arg Ser Arg Arg  
755 760 765

Thr Ile Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe Thr Val  
770 775 780

Asn Pro Val Asn Asp Ser Leu His Pro Val Gly Gly Leu Tyr Glu Ile  
785 790 795 800

Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Met Glu Glu Phe Ile Gln  
805 810 815

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820 825 830

Asp Tyr Ala Ala Cys Lys Ser Gln Leu Val Glu Tyr Gly Ser Phe Cys  
835 840 845

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850 855 860

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Thr Lys Leu Lys Asp Gly Phe Asn Phe Asn Val Asp Asp Ile Asn Phe  
885 890 895

Ser Pro Val Leu Gly Cys Leu Gly Ser Glu Cys Asn Lys Val Ser Ser  
900 905 910

Arg Ser Ala Ile Glu Asp Leu Leu Phe Ser Lys Val Lys Leu Ser Asp  
915 920 925

Val Gly Phe Val Asp Ala Tyr Asn Asn Cys Thr Gly Gly Ala Glu Ile  
930 935 940

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945 950 955 960

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